PCT

#10

RAW SEQUENCE LISTING DATE: 02/11/2003
PATENT APPLICATION: **US/10/009,030A** TIME: 14:33:45

Input Set : **A:\Bml41018.app**
Output Set: **N:\CRF4\02112003\J009030A.raw**

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  3 <110> APPLICANT: ARAND, MICHAEL
  4       ARCHELAS, ALAIN ROBERT
  5       BARATI, JACQUES
  6       FURSTOSS, ROLAND
  8 <120> TITLE OF INVENTION: EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN
 10 <130> FILE REFERENCE: bml-410.018
 12 <140> CURRENT APPLICATION NUMBER: 10/009,030A
C--> 13 <141> CURRENT FILING DATE: 2002-12-20
 15 <150> PRIOR APPLICATION NUMBER: PCT/FR00/01217
 16 <151> PRIOR FILING DATE: 2000-05-05
 18 <150> PRIOR APPLICATION NUMBER: FR 99/05711
 19 <151> PRIOR FILING DATE: 1999-05-05
 21 <160> NUMBER OF SEQ ID NOS: 8
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1197
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Aspergillus niger
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(1194)
 34 <400> SEQUENCE: 1
 35 atg tcc gct ccg ttc gcc aag ttt ccc tcg tcg gcg agc att tcg cct   48
 36 Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
 37   1               5                  10                  15
 39 aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa   96
 40 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
 41              20                  25                  30
 43 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg   144
 44 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
 45          35                  40                  45
 47 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg   192
 48 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
 49      50                  55                  60
 51 cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga   240
 52 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 53  65                  70                  75                  80
 55 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att   288
 56 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
 57                  85                  90                  95
 59 cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca   336
 60 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
 61              100                 105                 110
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63 ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg   384
64 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
65         115                 120                 125
67 cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg   432
68 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
69     130                 135                 140
71 gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg   480
72 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
73 145                 150                 155                 160
75 gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg   528
76 Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
77                 165                 170                 175
79 atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat   576
80 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
81             180                 185                 190
83 att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc   624
84 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
85         195                 200                 205
87 aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc   672
88 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
89     210                 215                 220
91 ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga   720
92 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
93 225                 230                 235                 240
95 atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt   768
96 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
97                 245                 250                 255
99 act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca   816
100 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
101             260                 265                 270
103 tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc   864
104 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
105         275                 280                 285
107 ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg   912
108 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
109     290                 295                 300
111 gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act   960
112 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
113 305                 310                 315                 320
115 gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att   1008
116 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
117                 325                 330                 335
119 cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg   1056
120 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
121             340                 345                 350
123 cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat   1104
124 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
125         355                 360                 365
127 cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg   1152
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128 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
129     370                 375                 380
131 aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag       1197
132 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
133 385                 390                 395
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 398
138 <212> TYPE: PRT
139 <213> ORGANISM: Aspergillus niger
141 <400> SEQUENCE: 2
142 Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
143   1               5                  10                  15
145 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
146              20                  25                  30
148 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
149          35                  40                  45
151 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
152      50                  55                  60
154 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
155  65                  70                  75                  80
157 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
158                  85                  90                  95
160 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
161              100                 105                 110
163 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
164          115                 120                 125
166 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
167      130                 135                 140
169 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
170 145                 150                 155                 160
172 Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
173                 165                 170                 175
175 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
176              180                 185                 190
178 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
179          195                 200                 205
181 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
182      210                 215                 220
184 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
185 225                 230                 235                 240
187 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
188                 245                 250                 255
190 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
191              260                 265                 270
193 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
194          275                 280                 285
196 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
197      290                 295                 300
199 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
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```
200 305                 310                 315                 320
202 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
203                 325                 330                 335
205 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
206             340                 345                 350
208 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
209         355                 360                 365
211 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
212     370                 375                 380
214 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
215 385                 390                 395
218 <210> SEQ ID NO: 3
219 <211> LENGTH: 21
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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227 atgcgatcgg actgctggac a                                          21
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231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
238 <400> SEQUENCE: 4
239 cgcgggcaat ccacacctac                                           20
242 <210> SEQ ID NO: 5
243 <211> LENGTH: 35
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
250 <400> SEQUENCE: 5
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254 <210> SEQ ID NO: 6
255 <211> LENGTH: 24
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
262 <400> SEQUENCE: 6
263 ttgaattccc tacttctgcc acac                                      24
266 <210> SEQ ID NO: 7
267 <211> LENGTH: 32
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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274 <400> SEQUENCE: 7
275 gctgaattca catgtccgct ccgttcgcca ag 32
278 <210> SEQ ID NO: 8
279 <211> LENGTH: 44
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
285 oligonucleotide
287 <400> SEQUENCE: 8
288 ccatgggaat tctcgagatc taagcttatg catcagctgc atgg 44

VERIFICATION SUMMARY DATE: 02/11/2003
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Input Set : **A:\Bml41018.app**
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date